

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: BEAUDOIN, Adrien R.
SÉVIGNY, Jean

(ii) TITLE OF THE INVENTION: ATP-DIPHOSPHOHYDROLASES, PROCESS
OF PURIFICATION THEREOF AND PROCESS OF PRODUCING THEREOF BY
RECOMBINANT TECHNOLOGY

(iii) NUMBER OF SEQUENCES: 8

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: GOUDREAU GAGE DUBUC & MARTINEAU WALKER
(B) STREET: 800 PLACE VICTORIA, SUITE 3400
(C) CITY: MONTREAL
(D) STATE: QUEBEC
(E) COUNTRY: CANADA
(F) ZIP: H4Z 1E9

(v) COMPUTER READABLE :

(A) MEDIUM TYPE: DISKETTE 1.44
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: WINDOWS 3.1
(D) SOFTWARE: WORDPERFECT 6.1

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: APRIL 10, 1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION: U.S.S.N 08/419,204
(B) FILING DATE: APRIL 10, 1995

(viii) ATTORNEY/AGENT INFORMATION:

09781796-024201

(A) NAME: Jean H. DUBUC, Gaétan PRINCE, Alain M.
LECLERC
(C) REFERENCE/DOCKET NUMBER: DH/10857.146

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (514) 397-4335
(B) TELEFAX: (514) 397-4382

(2) INFORMATION FOR SEQ ID NO: 1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 510 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1

Met	Glu	Asp	Thr	Lys	Glu	Ser	Asn	Val	Lys	Thr	Phe	Cys	Ser	Lys	15
				5					10						
Asn	Ile	Leu	Ala	Ile	Leu	Gly	Phe	Ser	Ser	Ile	Ile	Ala	Val	Ile	30
				20					25						
Ala	Leu	Leu	Ala	Val	Gly	Leu	Thr	Gln	Asn	Lys	Ala	Leu	Pro	Glu	45
				35					40						
Asn	Val	Lys	Tyr	Gly	Ile	Val	Leu	Asp	Ala	Gly	Ser	Ser	His	Thr	60
				50					55						
Ser	Leu	Tyr	Ile	Tyr	Lys	Trp	Pro	Ala	Glu	Lys	Glu	Asn	Asp	Thr	75
				65					70						
Gly	Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	90
				80					85						
Ile	Ser	Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	105
				95					100						
Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	120
				110					115						
His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	135
				125					130						
Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	150
				140					145						
Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	165
				155					160						

09781796-021201

Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile	170	175	180
Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp	185	190	195
Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly	200	205	210
Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro	215	220	225
Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg	230	235	240
Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys	245	250	255
Tyr Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile	260	265	270
Gln Val Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro	275	280	285
Gly Tyr Lys Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro	290	295	300
Cys Thr Lys Arg Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu	305	310	315
Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu	320	325	330
Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe	335	340	345
Asn Gly Ile Phe Leu Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe	350	355	360
Ser Ala Phe Tyr Phe Val Met Lys Phe Leu Asn Leu Thr Ser Glu	365	370	375
Lys Val Ser Gln Glu Lys Val Thr Glu Met Met Lys Lys Phe Cys	380	385	390
Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala Gly Val Lys	395	400	405
Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr Ile Leu	410	415	420
Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp Glu	425	430	435
His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp	440	445	450
Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu	455	460	465
Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu	470	475	480

09781796-021201

Met	Val	Leu	Phe	Ser	Leu	Val	Leu	Phe	Thr	Val	Ala	Ile	Ile	Gly
				485					490					495
Leu	Leu	Ile	Phe	His	Lys	Pro	Ser	Tyr	Phe	Trp	Lys	Asp	Met	Val
				500					505					510

(2) INFORMATION FOR SEQ ID NO: 2

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1818 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2

ACCACACCAA	GCAGCGGCTG	GGGGGGGGAA	AGACGAGGAA	AGAGGAGGAA	50
AACAAAAGCT	GCTACTTATG	GAAGATACAA	AGGAGTCTAA	CGTGAAGACA	100
TTTTGCTCCA	AGAATATCCT	AGCCATCCTT	GGCTTCTCCT	CTATCATAGC	150
TGTGATAGCT	TTGCTTGCTG	TGGGGTTGAC	CCAGAACAAA	GCATTGCCAG	200
AAAACGTTAA	GTATGGGATT	GTGCTGGATG	CGGGTTCTTC	TCACACAAGT	250
TTATACATCT	ATAAGTGGCC	AGCAGAAAAG	GAGAATGACA	CAGGCGTGGT	300
GCATCAAGTA	GAAGAATGCA	GGGTAAAGG	TCCTGGAATC	TCAAAATTTG	350
TTCAGAAAGT	AAATGAAATA	GGCATTACC	TGACTGATTG	CATGGAAAGA	400
GCTAGGGAAG	TGATTCCAAG	GTCCCAGCAC	CAAGAGACAC	CCGTTTACCT	450
GGGAGCCACG	GCAGGCATGC	GGTTGCTCAG	GATGGAAAGT	GAAGAGTTGG	500
CAGACAGGGT	TCTGGATGTG	GTGGAGAGGA	GCCTCAGCAA	CTACCCCTTT	550
GACTTCCAGG	GTGCCAGGAT	CATTACTGGC	CAAGAGGAAG	GTGCCTATGG	600
CTGGATTACT	ATCAACTATC	TGCTGGGCAA	ATTCAGTCAG	AAAACAAGGT	650
GGTTCAGCAT	AGTCCCATAT	GAAACCAATA	ATCAGGAAAC	CTTTGGAGCT	700
TTGGACCTTG	GGGGAGCCTC	TACACAAGTC	ACTTTTGTAC	CCCAAAACCA	750
GACTATCGAG	TCCCCAGATA	ATGCTCTGCA	ATTTGCGCTC	TATGGCAAGG	800
ACTACAATGT	CTACACACAT	AGCTTCTTGT	GCTATGGGAA	GGATCAGGCA	850
CTCTGGCAGA	AACTGGCCAA	GGACATTCAG	GTTGCAAGTA	ATGAAATTCT	900
CAGGGACCCA	TGCTTTCATC	CTGGATATAA	GAAGGTAGTG	AACGTAAGTG	950
ACCTTTACAA	GACCCCCTGC	ACCAAGAGAT	TTGAGATGAC	TCTTCCATTC	1000
CAGCAGTTTG	AAATCCAGGG	TATTGGAAAC	TATCAACAAT	GCCATCAAAG	1050
CATCCTGGAG	CTCTTCAACA	CCAGTTACTG	CCCTTACTCC	CAGTGTGCCT	1100
TCAATGGGAT	TTTCTTGCCA	CCACTCCAGG	GGGATTTTGG	GGCATTTTCA	1150
GCTTTTACT	TTGTGATGAA	GTTTTTAAAC	TTGACATCAG	AGAAAGTCTC	1200
TCAGGAAAAG	GTGACTGAGA	TGATGAAAAA	GTTCTGTGCT	CAGCCTTGGG	1250
AGGAGATAAA	AACATCTTAC	GCTGGAGTAA	AGGAGAAGTA	CCTGAGTGAA	1300

09781796-021201

(2) INFORMATION FOR SEQ ID NO: 3

(A) LENGTH: 11 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly
5 10

(2) INFORMATION FOR SEQ ID NO: 4

(A) LENGTH: 5 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

Leu Leu Arg Met Glu
5

(2) INFORMATION FOR SEQ ID NO: 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5

Ala Asp Lys Ile Leu Ala Asn Xaa Val Ala Ser Ser Ile
5 10

(2) INFORMATION FOR SEQ ID NO: 6

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6

Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile
5 10

(2) INFORMATION FOR SEQ ID NO: 7

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7

Lys Ser Asp Thr Gln Glu Thr Tyr Gly Ala Leu Asp Leu Gly Gly
5 10 15
Ala Ser Thr Gln Val
20

00781796-021201

(2) INFORMATION FOR SEQ ID NO: 8

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 AMINO ACIDS
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8

Lys Ser Asp Thr Gln Glu Thr Tyr Gly Ala Leu Asp Leu Gly Gly
 5 10 15
Ala

09781796-021201
T02T20-967E260